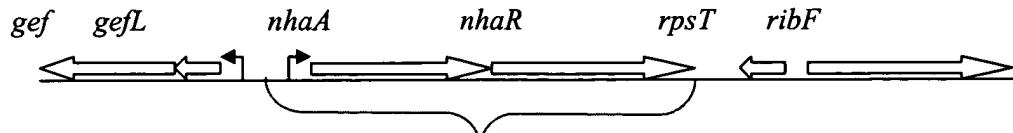
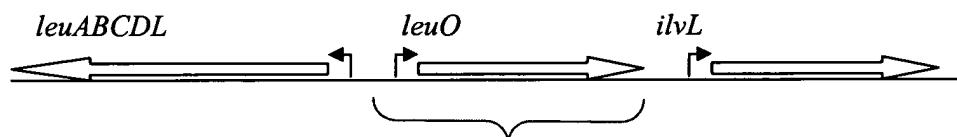


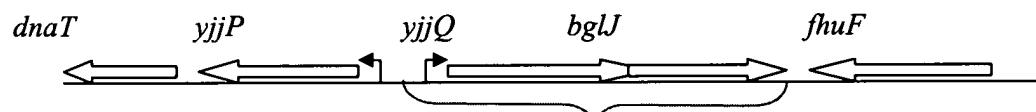
Figure 1



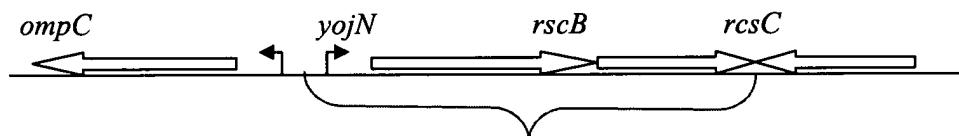
Genome included in cloning *nhaR*



Genome included in cloning *leuO*



Genome included in cloning *yjjQ*



Genome included in cloning *yojN*

Open reading frames or coding regions (↔);
predicted promoters (↑→);
cloned regions (└─┘)

Figure 2

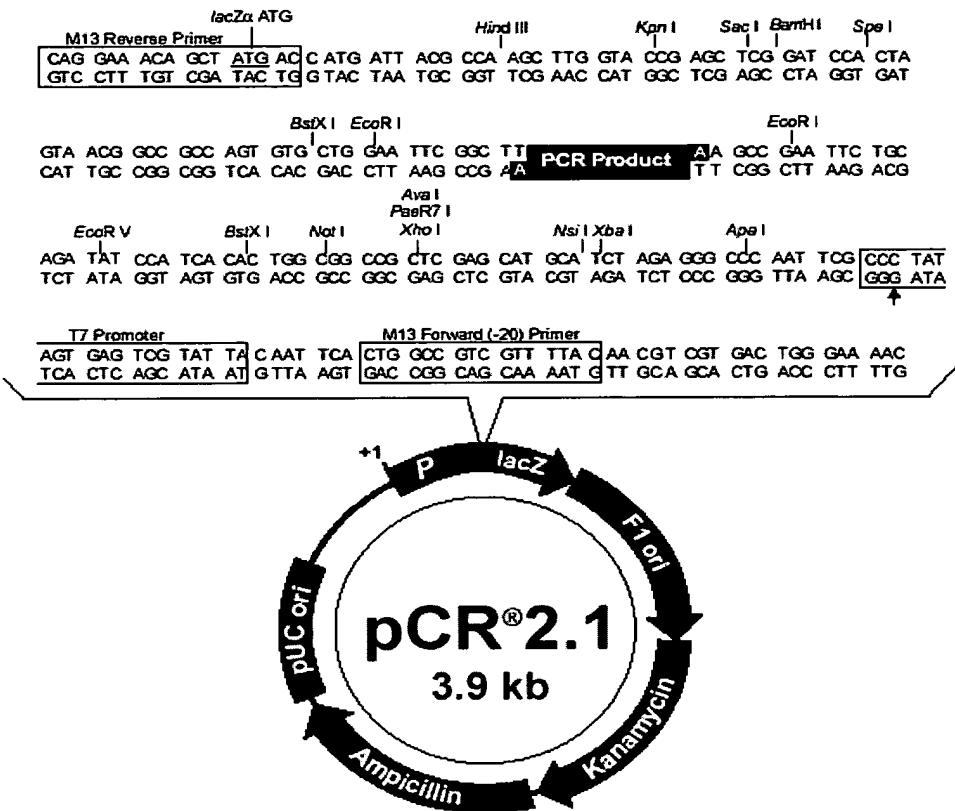


Figure 3

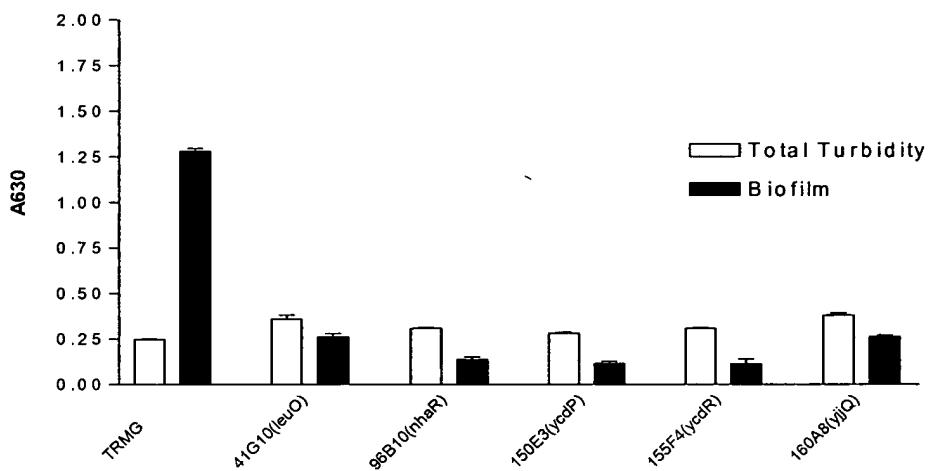


Figure 4A

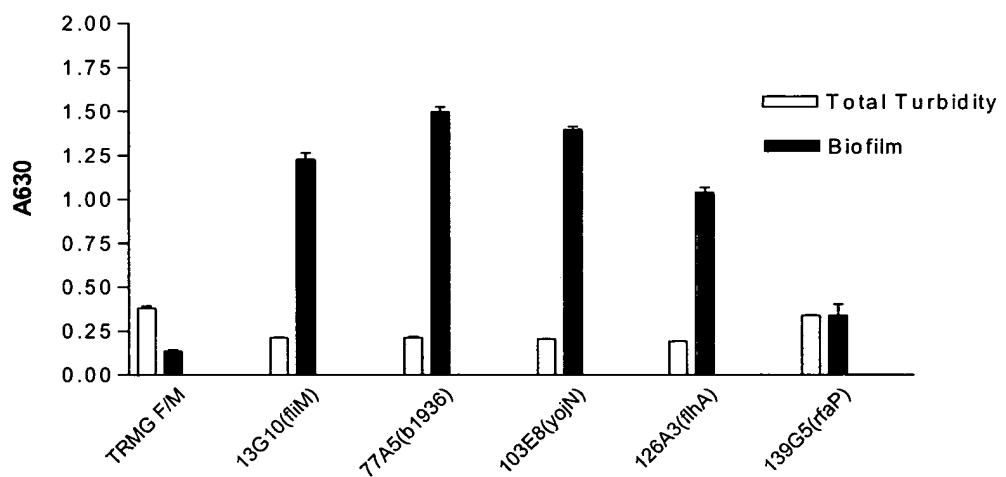


Figure 4b

Figure 5-1

1B10 (10X)

fliD gene - flagella biosynthesis; filament capping protein, enables filament assembly

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

```
AAAAACGGTTACCGGATCCGGATCATATGACAAGATGTATCCACCTTAACCTAATGATTITACCAAAATCATTAGGGG
ATTCACTCAG
GGTCAGGTCTGGATTTAAGTCCATCCTGATAGCCTCACCGCCCGCAAAAGC
GACGCTAACCCCCATTCAAATCAGCAATCGTCGTTACCGCTAAACTAGCGCC
TACGGTACGCTGAAAAGCGCGCTGACGACTTCCAGACCGCCAATACTGCATTGT
CTAAAGCCGATCTTTCCGCCACCAGCACCAAGCAGCACCAACCGCGTTC
```

Figure 5-2

12E12-6 (7x)

rfaG gene - enzyme, macromolecule metabolism; glucosyltransferase I, LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # S75736

Protein Accession # AAD43826

```
AAAAACGGTTACCGGATCCGG
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTITACCAAAATCATTAGGGGATTCACTCAG
AGTTAAGTCCCATAACCAACCATGGACGCAATGCAGAATATTATGCCTGGGTACAAATCATCTCAA
AGAGCATCCCGCAGATCGCGTTGGGTTAATAAGATGCCTGGCCTGGATGTTATTTGCCGC
TGATGTTGTTACGCCGAGAAAGITGCGCAAGAAAAAGGTTTATATCGTTAACATCACGATA
TCCNCNNNNNNNGTACTAGTCGACGCCGGGCAANNN
```

Figure 5-3

13G10-4 (11X)

fliM gene - Structural component; surface structures/flagellar biosynthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

```
NAAAAACCCGCCGACATCCGGATCCGG
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTITACCAAAATCATTAGGGGATTCACTCAG
TGTTCAACCTGCTGCGTGTAGCCCGGATATCCNNNCNCNGNACTAGTCGACGCCGTGGCCA
```

Figure 5-4

14C10-4 (10X)

flgE gene – structural component; surface structures/ flagellar biosynthesis, hook protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74160

```
AACGGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGATTATCAG
AGATCANCCTGAATTCCAGTGTACCGCTTCCTACTGTTACGCCATTCAANNGCCNGCAATGCGGNTANCTNTN
ACAAANAAGGTTNNGTGACTGTTTCCACAGTCATGGTAATGCTCATGACATGAGCGTCTACTTGTGNACC
CGGGGATAATAACTGGCAGGTCTACACCCAGGATAGCAGTGATCCAACAGCATTGCGAAGACACCG
```

Figure 5-5

36E2-5 (3X)

yhjH gene (complement) - orf; unknown function ; hypothetical protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_004431

Protein Accession # NP_417982

```
AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGATTATCAG
TGCTTACACCTGGCAGCCGATCTATCAAACATGCGGGCGGTTAATGGCCGTGGAGCTATTAACGGT
GGTCACCGCATCCCTTGAACCCCTCGCAACGCCGCGCCGGATCGCTATTTACTGAAATCACCCT
CAGCCATCGGATGGAGGTTGTGAAAAGAGCAGATTGATTGCTGGCGCAAAAGCCGACTTCTTAT
AGAGCACGGCCTGCTGGCATCGGTCAATAT
```

Figure 5-6

38G7-2 (11X)

fliM gene - Structural component; surface structures/flagellar biosynthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

```
AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGATTATCAG
CTTCAAGCGCCAGTTCAACATGCGGTTGATGACCGCGTTCGGTATGGTAAACTCGCGACCTT
CCACTTGGTCGGGAAGCGTCCATGCCGCCAACAGGTTATCCACGGCGATAAACACCCAGACTC
GGTGAGAACACCACCAGCCCAGTGCCGCGCAGCGGTTTCAGATGGATAAGGTTCAGGGTGGTCGG
CACCGGCAGGTTGCGGGCAAATTATGGTACGGCTGAATGCGGATGGCCCCGACGGTTATATCCN
GNCCNNNNNTACTAGTCGACG
```

Figure 5-7

39C9-2 (3X)

rep gene - enzyme; DNA replication, repair restriction/modification; product - rep helicase, a single-stranded DNA dependent ATPase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000454

Protein Accession # AAC76783

```
AAACGGTTACGGATCCGGATCATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATT  
CATCAG  
TATCCAGCCCCAACGTATGGAAAGTGGAGATCATCAGCCCACGCCCTTTGCGCCCCAGCGTCT  
GCCCTACACGCTTTCATCTCGCGCGCTGCTTATTAGTAAAGGTACCGCCGCAATGTGCCGCG  
CCTGATAACCGCAACCGCGGATCAGATGGCGATTATTGGTATAACACCGAGTTACCGGAAC  
CCGCGCCGCCAGCACCAAGGCAGGGCCGTAACGAATTGACAGCTTGTGTTGCCGGGTTT  
AGACGCATAGGTGTATTGCTA
```

Figure 5-8

42G6-4 (12X)

fliP gene – putative structure; surface structures/ flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

```
CGGNCCGGATCCGG  
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTACATCAG  
TGGTACGCATCTACATAAATTTGTCGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGC  
CAGCCCCAGCAATACCTGGTTAGGTGGCGCGGGAGGGTGTCCAGCGCTTACGCAATAAAC  
AAAAACAATGATGATGCGGGTAAACTGGTCATCATCAGTAAATTGCCGGAATAAACGTCAACG  
AGGTGATGAACACCAAGCGTCTGCACCGGGAGC
```

Figure 5-9

43B10-3 (11X)

fliG gene – Structural component; surface structure, flagella motor component

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75006

```
NNCNNAACANACGGNNCCGGCNG  
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTACATCAG  
CGGCGAGCTGGCGCAGAAAATCATCGACGAGATGTTCTGTTGAGAATCTGGTGGATNTCGCCAATCGCN  
GTACTAGTCGACGNGTGGCCAANTGGATTCCNAATCGCTGNTGATCGCGCTGAAAGGAGCCGAGCNGTC  
ACTGTGCNAGAANTTCTGCNCNATATGTCGCNNCGTGGCGCCNATATCCCNCCNACCGTACCCCTNGN  
ACGNNNNACCGNACCCNNTNCGGNCAAGNATGNNANNANCCNGATANANCAGNNCANTNNGATN  
CACNNNATANNANNGNCGCCNAC
```

Figure 5-10

43F5-2 (2.5X)

wecB gene - enzyme; Central intermediary metabolism; sugar-nucleotide synthesis, product - UDP -N-acetyl glucosamine-2-epimerase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000455

Protein Accession # AAC76791

```
AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG
GGTCAGGCATGCTCTCGCATTCTGGAAGCGTAAAAAATAATCGGATATCACTATGAGTTTGCGA
CCATTCTGTTATCGGACTGGTTATATCGGGCTGCCAACNGCTACNCGACNCGCGCCNCGGCAA
AACAGGTAATTGGTGTGCGATATCAACCAACATGCGGTTGATACCATCAATCGTGGCCAAATCCATA
TCCCCCCCCCCCCGTACTAGTCGACG
```

Figure 5-11

45C8-4 (4X)

frdA gene – enzyme; energy metabolism, carbon: anaerobic respiration; product is fumarate reductase, anaerobic flavoprotein subunit

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000487

Protein Accession # AAC77114

```
CGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG
TGCCCGCAGCGCAAATCCGAATGCAAAATCGCACTAATCTCAAAAGTATACCCGATGCGTAGCCATACC
GTTGCTGCAGAACGGGGCTCCGCCCTGTCGCGCAGGATCATGACAGCTTCGAATATCCCNCCCGT
ACTAGTCGACGCCGTGAANANNNN
```

Figure 5-12

49G9-3 (12X)

fliP gene - putative structure; surface structures, flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

```
AACGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG
GGCGCAGCCGCTCGCTGAGTTATGCTCGCTCAGACCCGTGAGGCAGATTAGGGTTGTTGCCAG
ACTGGCGAATATCGGCCGTTGCGTNCTACTCNACNCGTGCCATGCGCATTTGCTNCCNGCCTA
CGTGACCAAGCGAGTTGAAACCGCATTCAGATACGGCTTCACAGATTTCATCCCTTTTGATTTA
TCGACCTGGTGTAGCCAGCGTGTGATGGC
```

Figure 5-13

51B12-3 (6X)
fliM gene - flagella gene, flagella biosynthesis; motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

```
ATGAAAACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGGATTATCAG
TACTCAACTTCCAGCGGATTAATCGCCTTCCAGGCCTCGCTATAGCCTCAAGCGCCAGTTCAAC
ATGCGGTTGATGACCGCGCTGTTCGGTATGGGTAACACTCGCGACCTCCACTTTGGTCGGGAAGCGT
CCATCGCCGCCAACAGGTTATCCACCGCGATAAACACCCAGACTCGGTGAGAA
```

Figure 5-14

57E7-6 (7X)
fliP gene - flagella gene, putative surface structure, flagella biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

```
CGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGGATTATCAG
GGCGCAGCCGCTCGGTGAGTTATGCTCGCTCAGACCCGTGAGGCAGATTAGGGTTGTTGCCA
GAATGGCGAATACCGGCCCGTTGCAGGGACCTGAAGCCGTGCCGATGCGCATTTGCTCCGGCCT
ACGTGACCAGCGAGTTGAAAACCGCATTTCAGATAGGCTTCACGATTTCATCCCTTTGATTAT
CGACCTGGTGATAGCCAGCGTGTGATGGCATTGGGATGATGGTT
```

Figure 5-15

61G2-3 (10X)
255 bp down stream of flhB gene

Transposon Tn10 Accession # AY528506

Nucleotide Accession # U88319

Protein Accession # AAC17834

```
NGNNNATACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGGATTATCAG
TATTAAGCGTGATGATGCCAGAGCGCAAAGCGTTCAATGGTTGAGTAAGGGGCAAAACAGGCG
GGATTAGGGTTTGCTGCCACATATCCNNNNNNNGTACTAGTCGACCGTGGCCA
```

Figure 5-16

63A9-1 (4X)

rfaQ gene (complement) – enzyme, macromolecule metabolism, LPS; LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_002695

Protein Accession # NP_312534

AAACGGNCGGATCCGG
GATCATATGACAAGATGTGATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGGATTATCAG
TATGTGTACCGTGTATTGGCGCTAAGNGTGNAGCTTTTCCAANTACCATGCTTGCNNATG
ACCATAANGTTGCGATATNTTCATTCCGTGCATGCAAACANCGTACCCNNCAGCGCCACCATNCAC
TGATGCGTCNGANTAATGACCAGGTNTANTTATTCTNTGCCCGAGCCTCATCANCNAANGCTCN
CTTNTNNNCGGNANNNNATTTNCCNGTCTNNNTNTGNTTNANTNNNTACCGGGCNACNNA
TTNGTNTGGTCNTACGNGCENNATAACNGCENNCTCNCNNCC

Figure 5-17

64F2-1 (9X)

factor Sigma32 – promoter dnaKp2; documented +1 site at 12121

Transposon Tn10 Accession # AY528506

Nucleotide Accession # D10765

Protein Accession # BAA01595

CGNCGGATCCGG
GATCATATGACAAGATGTATCCACCTAACCTAATGATTITACCAAAATCATTAGGGGATTCATCAG
CGTTTCCGCCCCCTATTACAGACTCACAAACCACATGATGACCGAATATATAGTGGAGACGTTAGATG
GGTAAAATAATTGGTATCGACCTGGGTACTACCAACTCTTGTAGCGATTATGGATGGCACCACT
CCTCGCGTGCCTGGAGAACGCCGAAGGCATGCACCACGCCCTCTATCATTGCCTATACCCAGGAT
GGTGAACACTCTAGTTGGTCAGCCGGTAAACGTCAGGCAGTGACGAACCCGCAAAACACTCTGTT
TGCGATTAAACGCCCTGATTGGTCGCCGTTCCAGGACGAAGAAGTACAGCGTGATGTTCCATCAT
GCCGTTCAAAATTATTGCTGCTGATACTCCNCCCCCCNNG

Figure 5-18

66F4-3 (10X)

fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

TACCGGATCCGG
GATATATGACAAGATGTATCCACCTTAACCTAACCTAATGATTTACCAAAATCATTAGGGGATTATCAG
CTTCAAGCGCCAGTTCAACATGCGGTTGATGACGCGCTGTCGGTATGGTAAACTCGCGACCTT
CCACTTTGGTCGGGAAGCGTCCATCGCCGCCAACAGGTTATCCACGGCGATAAACACCAGACTC
GGTGAGAACACCACCAGCCCAGTGCCCGCAGCGGTTTCAGATGGATAAGGTTCAGGGTGGTCGG
CACCGGCAGGGTTCGGGCAAATT

Figure 5-19

67C8-4 (6X)
fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75012

```
NNCGTNCGG
GATATTGACAAGATGTATCCACCTTAACCTAATGATTTCACAAAATCATTAGGGGATTCATCAG
CGCTTGAAGGCTATAGCGACGCCTGGAAGGCCTTAATCCGCTGGAAGTTGAGTACGTGCGTTCG
GAAATGCAGGTGAAATTACCAATATCACCACCTCGCCGAACGACATTGTGGTTAACACGCCGTT
CATGTGGAGATTGGCAACCTGACCGCGAATTAAATATCTGCCTGCCATTTCAGCATGATCGAGCCG
CTACGGGAATTGTTGGTTAACCCGCC
```

Figure 5-20

67C9-6 (8X)
fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75012

```
ANCGGATCCGG
GATATATGACAAGATGTATCCACCTTAACCTAATGATTTCACAAAATCATTAGGGGATTCATCAG
CGCTTGAAGGCTATAGCGACGCCTGGAAGGCCTTAATCCGCTGGAAGTTGAGTACGTGCGTTCG
GAAATGCAGGTGAAATTACCAATATCACCACCTCGCCGAACGACATTGTGGTTAACACGCCGTT
CATGTGGAGATTGGCAACCTGACCGCGAATTAAATATC
```

Figure 5-21

67E10-5 (6.5X)
fliI gene -Enzyme, flagella synthesis; surface structures, flagellum specific ATP synthase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75008

```
CGNCCGGATCCGG
GATCATATGACAAGATGTATCCCTTAACCTAATGATTTCACAAAATCATTAGGGGATTCATCAG
CACCTGCATTGCAGGAGCGGAGAAACATCCGCCGGAGCGGCAATCACCCTGAGCGTGCACGCCCTCG
GCACCGAGGATGTTCTCAATAAAATCTTACTTCGCGCCACGTTACCAATCAAACCCACGACAATGATA
TCCNNNNNNNNNGTACTAGTCGACCGTGGCCAAT
```

Figure 5-22

70G12-5 (5X)

fil gene – flagella synthesis, enzyme: surface structures; flagellum specific ATP synthase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75008

TANGAAAAACGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTTCATCAG
CGCTCCAGCCCCCTGGAGAGACGCTTNCCAGTCCCGCGCGTTCAAAAATGCCTTGTGCAAATAGCCCTCCAG
CTGCGGCCACAGGGCGATGGCTTATCGAGCATGGATCGCTGCCCTTGGCATACGCCCGACGCTAACCA
GATCGCGGTTACGCTGAAAACTCGACAACAGCTGTTGAAGGTGCGCACTCGCGCGTAATGTTGCTCACTG
ATCAACGCCGTATTGCGCGCTGATCGACGCTTAATATCCNNNNNNNNGTACTAGTCACGCGTGGCC
A

Figure 5-23

71A4-3 (10X)

Downstream of rfaQ gene

Transposon Tn10 Accession # AY528506

Nucleotide Accession # M80599

Protein Accession # NP_418089

AGCNCGGGACNTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTTCATCAG
AGTCGCTAGTGGAAAAGCCATTTCGAAAAATCCTGGTCATAAAGATGCGATATCCCCCCCACCGCGT
ACTAGTCGACGCCGTGGCCANANANNNNNNNCGGCANNCCNCCNT

Figure 5-24

74B5-2 (2.5X)

rfaG gene (complement)- enzyme, macromolecule metabolism, LPS; glucosyltransferase I, LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # S75736

Protein Accession # AAD43826

ATACCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTTCATCAG
CGCATTGCAACAGTTGCCGACGGGGCCACCATGTTGGGTATATACACAGTCGTGGGAAGG
CGATTGCCCGAAAGCATTGAGCTTATTCANGNGCCAGTTAAGTCCNTACCAACCATGGACGCAA
TGCAGAAATTATGCCTGGGTACAAAATCATNTNAAACAGCNTCCNCAGGATCTGTGCGNNGN
GTTCAATTATTATNCCCTCGNCNGGATTATCTTATTCGCTGCTNAATGTCNGTCTTCTNATTCTA
AATNT

Figure 5-25

76F11-2 (5.5X)

fliM gene - flagella gene, flagella motor switch biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # [AE000286](#)

Protein Accession # AAC75012

```
NGAAAACGGNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCA  
CGCTTGAGGCTATAGCGACGCCCTGGAAGGCGATTAATCCGCTGGAAGTTGAGTACGTGCGTT  
GAAATGCAGGTGAAATTACCAATATCACCACCTGCCAACGACATTGTGGTTAACACGCCGTT  
CATGTGGAGATTGGCAACCTGACCGCGAACCTTAATATCTGCCTGCCATTCA  
GCA
```

Figure 5-26

77A5-2 (11X)

b1936 gene - orf; unknown function; hypothetical protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC 000913 (genome)

Protein Accession # E64957

```
CNCGATCCGG  
GATCATTGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCA  
ATTCAAGGTGCGTAATAAGCTGGTGGCGCGTATCAGGAAGTGTGAGCATGCAGGTGAGGTT  
GTAACCTGTTGTTAATTACATCCGATCTCACCGCGTGGGGCATGGATGGGCAA  
ACTCAATT  
TCTGGTTAAATGGATAACCTGATCCTGAACGTTCTGCCATCCACGATCCGTATACCGGATAAC  
CCCCCTGAACATCAGAGCGTCTCA
```

Figure 5-27

78E3-2 (7X)

fliA (complement) - flagella biosynthesis, alternative sigma factor

Transposon Tn10 Accession # AY528506

Nucleotide Accession # [AE000285](#)

Protein Accession # AAC74989

```
NAAAACGNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCA  
GGGTTAATACCAAGTTTCGCGCTCCGGCAACGTTTCGATGGCTTCATCACCGCTGGCGCAGAT  
TACTGTCCAGTAGTTGTTGAGCGGGTTCTCGCTGATGATCATCAGTAACCAGTTGATGCTATC  
GCCGTGCTCTCGCGCCACTCATCGTAGGAGAAGAGCTGGCTGTTATTGGTGTGAGCAACATTG  
GCGATAATCGGCAATATCNNCCCCCGTACTAGTCGACCGTGGCCAA
```

Figure 5-28

78F6-3 (2X)

tolA gene - membrane; colicin-related functions; membrane spanning protein required for outer membrane integrity

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000177

Protein Accession # AAC73833

```
ATACNCGACCGG
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
AGTTTAGCTGCTGCCAACGCAGCCTGACAAAGTGCAGGATGCCACCTCAGGTTGATATCCAGT
AACATACCATCGGGTGCCAGTTTATGCGCAGCGTACAGGTTTGCCTGCATAGGACGATGCGTCA
TAGAACTTACTTCGATAGCAGATTAACTGCCCCGCATAGTTATTGATATCCNCCCCCNNGTA
CTAGTCGACGCGTGGCCANNTATTNGATATCNCNCCNGCTANTCCNCGTGGNCATATCT
GATNC
```

Figure 5-29

85G11-1 (6.5X)

Between 2 promoters (complement) - 1) factor sigma 70; predicted +1 site at 201135 and 2) factor sigma 70; predicted +1 site 2011238

Transposon Tn10 Accession # AY528506

Nucleotide Accession # D89826

Protein Accession # AAC75005

```
ANNGNAANAGCNCGCCGGACATCCGGATCCGG
GATCATATGCACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
AGTCTTGNTCCACTTGCCAATANCGCCGCCNTAGCNCTAGNCNCAGACGCGTGG
CCA
```

Figure 5-30

89A8-3 (6.5X)

fliG gene - flagella structural; flagellar motor component

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75006

```
CGNTACCGGACCGG
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
TGCTCGGCTCCTTCAGCGCGATCAACAGCGATTGGAATCCACTCCTGCAACAGACGCTGAATG
CTGCGATCGTCGACATCCACCAAGATTCTGAAACAGGAACATCTCGTCGATGATTTCTGCGCCAGC
TCGCCGTCGAATTACCGCACGGCGGTAATAACGGCTTCTCCTGCTGAGTTTC
```

Figure 5-31

92G7-3 (3.5X)

rnhB gene – enzyme; degradation of RNA; product is RNase HII, degrades RNA of DNA-RNA hybrids

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000127

Protein Accession # AAC73294

```
GGAAAAAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
GGTTGGGTACCCCTTGTGTTGGCAAAACCATATTGCGGGAAAACAATATCCAGCGCCGCCNTNN
NGCGTCACGCGTNACTTCGCCAGGATAGACGCCGCACTGATTCGGTACCGGGCTATGCCCTT
CACCAACAGCCATCGCAGGCATCGGTAAATTCCGGCAGCGGTTACCATCAATCAACACATATTCCGG
CGCAATATGCAGCCCAGCGACGGCACGCGTGCATGCCAGCATGGTCGATGAAGAATGTTCAGCT
CGTCGATATCCNNNNNCNCGTACTAGTCGACGCGTG
```

Figure 5-32

92G9-1 (3.5X)

rnhB gene – same clone as above

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000127

Protein Accession # AAC73294

```
TANGAAAAAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
GGTTGGGTACCCCTTGTGTTGGCAAAACCATATTGCGGGAAAACAATATCCNCCNCCNNGTACT
AGTCGACGCGTGGCAAATATNNNNATATNNNNNNNNNNCTANNNNNCNCNGGGNNANN
N
```

Figure 5-33

94G6-3 (4X)

Downstream of rfaQ gene

Transposon Tn10 Accession # AY528506

Nucleotide Accession # M80599

Protein Accession # NP_418089

```
NNNGNAAAGCCGCCGGACNTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
AGTCGCTAGTGGAAAAGCCATTGCAAAATCCTGGTCATAAAGATGCGATATCCNGNNCCNNG
TACTAGTCGACGCGTGGCAAANNNCNCNNNNNNNNNATNCTNGCNCCNNCCANC
```

Figure 5-34

98E7-4 (6X)

fliR gene - putative enzyme, surface structures; flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75017

```
CGACCGGATCCGG
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGGATTCATCAG
CACTGAATCTGGCATTAGGTTACTTAATCGTATGGCCCCGCAATTATCCATTGGATTTCCATT
AACTCTGACTGTCGGCATCTCTTAATGGCGGATTAATGCCGTTATTGCACCTTTGCGAACATTATTTC
AGTGAAATTGCTGGCTGATATTATTAGTGAATTGCCATTAATATAATTCCGTAACGTTATCATG
TTATCCTAAGGATTATCCGAAAAATAACCTACGAACATCTCCAGGACTCCTGCAGCGAAATATTGT
TTAAGCTCACTCACATATCCNCCNCCNGTACTAGTCGACGCGTGGCCA
```

Figure 5-35

98E11-3 (5X)

flgH gene - structural component, surface structure; flagellar biosynthesis, basal body outer-membrane L (LPS layer) ring protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74163

```
AACNAACGGNTCCGCATCGG
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGGATTCATCAGC
GCTGCGCATACTTATGCCATATCCNNCNNGNNGTACTAGTCGACGCGTGGCCANATTNNNNNAT
CCNNNNNNNGGGGCNNN
```

Figure 5-36

98G12-4 (5X)

mdoG gene – enzyme, osmotic adaptation; periplasmic glucans biosynthesis protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000206

Protein Accession # AAC74132

```
AAACGACGGACCGG
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGGATTCATCAG
GGGGCAAGTTGCTTTGGCGTCTCGTAGCCTTCCCGCTAAAGATTGAGCTTGCTTGCACAT
CATCAACTGAAAGCCCAGCTTGAAGATGTATACAGGGTTAACATTACTGCAGCACTCAACCAA
CGCATTTCATTATTGTAGCTTATGTTCTAATTAGTAAGGCACCTCCCCCTTNGTGTGCTTATA
TCCCTNNGNTNNCNTNCTAGTCNACNCGTGGCCACTNCTATCCNGNNNTCCCGNTNNGCAGTANT
CAGAC
```

Figure 5-37

103C8-4 (9X)

fliP - flagella biosynthesis, surface structure

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

```

GANNAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTCAATCAG
GGCTGCGCCCTTTCCAGCGCCTCTGCATTGATATTTCTCTCGCTGAATGGCTGGTACGCAT
CTACATAAATTTGTCGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGCCAGCCCCAGC
AATACCTGGTTAGGTGGCGCGAGGGTGTCCAGCGCGTTACGCAATAAACCAAAACAATGAT
GATGCGGGTGAACACTGGTCATCATCAGTAAATTGCCGGAATAACGTCAACGAGGTGATGAACA
CCAGCGTCTGCACCGGGAGCGACCAGCTTGCCACCGCCAGGCAGCG

```

Figure 5-38

103E8-4 (7X)

yojN - putative regulator, not classified; product is putative 2 component sensor protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000310

Protein Accession # AAC75276

```

NATACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTACCAAAATCATTAGGGATTCAATCAG
GGTGCAACCTGTATCACACCCGATGAAAGATTAATTAGTCAGATTATGATATCTTTAACGGAT
AATCCGTCTAACCTTACTGCCCTGGCTTGGCTTTAACGCGATGATGAGTCTGGCGTACCGGGAAATT
GGGCCTGGTCAATTGTGCGTCAACTCAATATGAGCAACGCTATGCAGGAAGCGGTCTAACATTA
ATTGAAGTGCAACTGGCGCAGGAAGAGGTGACAGAACGCAATGCCCTGGCGGAGATGAAAATGCGC
AACTCCATGCCAGCGGCTATTATGCGCTTTGTAGACACAGTACCGGATGATGTTAAGAGGCTGT
ATACTGAAGCAGCAACCAGTGACTTGCTGCGTTA

```

Figure 5-39

104G4-5 (2.5X)

Between mreB and yhdA genes (complement). mreB: phenotype, cell division; regulator of ftsI, penicillin binding protein 3, septation function. yhdA: orf, function unknown, hypothetical protein, 1232 bp upstream of mreB

Transposon Tn10 Accession # AY528506

Nucleotide accession # M22055

Protein Accession # AAA83892

```

ANNNNCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTNATCAG
CTNAATGCATGCNCNACCATTGCCTCNGCTGTTGCAACCGNGTAAGGNGCATTCAATNTGCATATG
TTGCTGCNANCAATCTGGCTGAGNAGACAAGCNCACTCCATGANACGCATCGCGCATTATTNTAC
GTGAAANCGGATNNAANGGNTGGNTAAACCNANGANCCNCNCGCGANTATNNTCCNCTGCAN
NCTNANNTNGNCTNGNACNGANNNCNANNNCACNCCTTTNTNNNTCCGNTNNNGNNNNNN
NNNTNGTNTCCNNCTGTNTNCANNTNNCNGNTCTNCNCCTNTCCANTGCCANTTGTN
NCNAGGTNCGATNTCTGCNGACCACNNNTAGNANCCNN

```

Figure 5-40

107B12-2 (2.5X)

Upstream of promoter - factor sigma 70; predicted +1 site at 3806141

Transposon Tn10 Accession # AY528506

Nucleotide Accession # M80599

Protein Accession # AAC17834

```
GNAAANCCCGCCGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGGATTTACCAAAATCATTAGGGGATTATCAG
GCGGTAGCGTGTCTTCTGCTTAACCTAACAGACAATCACACACAAAAGAGTCGCTAGTGGAAA
GCCATTTGAAAAATCCTGGTCATAAAGATGCGATATCCNNNNNNN
```

Figure 5-41

110E8-3 (6X)

fliP gene – Putative surface structure, flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession #AE000287

Protein Accession # AAC75015

```
AACGCTNCCGATCCG
GATNATATNAACAGATNTGTATNCACCTTATCTTAATGAAATTACCAAAATCATTTGGGATATCATAT
ANGGGCTGCCCCCTTTCCAGCCCCCTACTGCATTGATATTTNTCTCGNTGNAT
GGCTGGTACGCATCTACATAANTNTGACGATCACCAGTGAACNTAATAAAANAG
GNCNNANNCACTGCCANTCCCAGCAATNCNTGGTTNNGTGGNGCGGACGGTGCT
NCCATNGCNGACNCACNNAACCNANNCAATGANGNTNCCNCNGANANTGGA
NATCATCCTGCAANNCAACNGNATNCNNA
```

Figure 5-42

110F12-2 (9X)

Between flhD and insB_5 genes (complement)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # U88319

Protein Accession # AAC17834, AAC74963

```
CGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGGATTATCAG
CGATNANCTGCAATAAGCAGAACNCCTTTGGNTTAATATGTCTTACAATAGAAATGGGTCTTACAC
TTATCTAAGATTTCTATATCNCNCNCNCGCCNGTACTAGTCGACCGGTGGCCATTATNNNNNATNTCCTN
NTNGTCTCNGNNNCNNCNCGCGCCNCANCNNNATATNNNTNNNNCNCTNCACTCTN
```

Figure 5-43

111G8-1 (4X)

flgK gene – structural component, flagella biosynthesis; hook-filament junction protein 1

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000209

Protein Accession # AAC74166

```
AACCCGATCCGG  
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTATCAG  
GGCTGGGTTGGCAATGGTGTCTACGTTCTGGTGTGCAGCGTGACTGCGTTATTACCAAC  
CAGTTACGTGCGCGCAGACGCAAAGTAGCGCTCTGACTGCCGCTATGACGAGATGTCGAAAT  
CGACAATATGCTCTCCACCAGTACCTCTCGCTGGCAACACAGATGCAGGATTCTTACCCAGCCT  
GCAAACGCTGGTGAAGTAACCGGAAAGACCCGGCAGCGCGCCAGGGCCTGATTGGAAATCAGAA  
GGATTGGTGAATCAGTTAAACACCACCGATCAATATCNCNNNNCCGTACTAGTCGACGCGTGG  
CCANANNATNCT
```

Figure 5-44

115A3-5 (2.5X)

fliD gene – flagella biosynthesis, surface structure; filament capping protein, enables filament assembly

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

```
ATACCNGATCCGG  
NTCATATGACAAGATGTATCCCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTATCAG  
GCTTACGCTGCTTTGCGTTGATGGCATACGGATCCGCTTAACGATGAGTTAGCCGCGCT  
GATATCAATGGTNATCGTACTANTCGACCGTGGCCATGAATGGTGAAGTTACTGTCGCTGGTGGC  
GATGCCGTTTCATATCGNCNNTNCNGTACTAGTCGACCGTGGCAAATTNNNTNANAAAAAA  
TTCN
```

Figure 5-45

115B7-6 (7X)

flgB gene – flagella biosynthesis, cell-proximal portion of basal-body rod

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74157

```
AACGGTTACCGGATCCGG  
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTATCAG  
CGCGCGATATCGATTTGCCAGTGAACCTAAAAAAAGTCATGCAACGTGGACGGGATGCAACCAGT  
GTGGTTGCACTGACGATGACCTCAACGCAACACATTCCGGCGCAGGGCCTGACGCCCTACCGCA  
GAACTGCAATACCGTATTCGGACCAGCCTCGCTGACGGTAATACCGTCGATATGGATCGCGAA  
CGCACCCAGTTGCCGATAACAGCCTGCAATACCAAGATGAGCCTAGCG
```

Figure 5-46

122F6-1 (4X)
fliL gene - flagella gene; putative surface structure

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75011

```
CGNTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG
CACGACGCGTTGCTGCGCTTGTGCGTACAGCGGCAACCTGATGCGAATGCCAGTAGCTGTAACCTGC
GCTGGCACAGGCCGCGAGGGTAATGAATACCAAGAATCGGGATCCAAAGCGATCGCTTGCTTCTTCTT
GCTTATCGCGTAATCAGTCATGTGTTGCGGTCTCCTGTGTCGCTACTGCTTATC
```

Figure 5-47

123B8-4 (3.5X)
rfaQ gene (complement) – Macromolecule metabolism, LPS; LPS core biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_002695
Protein Accession # NP_312534

```
AAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG
CGCTAAGTGTGTAAGCTTTTCCAAATACCATGCTGCCGATGACCATAAGTTGCGATATTTTC
ATCCGTGCAGGTAACAAACGTACCAGCAGCGCCACCATCCACTGATCCGTAAGATTAATGACCAAG
GTCATAATTATTCGCACGCAGAGNTTTATCAACNAAGCACATTAAATTNATCGAAAGTTCC
CNCNCCTTATTGCTTANCCATAGAGCGCANTNNTTCCGGTTTNCANACAAAATNTGGATGGT
GNCTGNCAAGCNNCANGTCTANNTNNGCTNTATGAGAATCTG
```

Figure 5-48

123E4-3 (6.5X)
fliR gene – putative enzyme; flagella biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000287
Protein Accession # AAC75017

```
AAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG
AGTTTACCCGTTTCCGGTACGCTGCCGCTCGCTCAGAATCGGCCGCGTGGAGATCATGCCAGCTCN
CGCANTNACGGNCAGAANTACAGGTTAACCAAGGATAGCCATTGTTNGCTGCCACCTGCANCAT
AGTACGGTTACCCNATGATTACTNGNAGGTTAGTGAACAANGTGCAGNCAGTNATTCAACAAACA
CATTNNGCATGNTCTGTCTNGGCANNTATTTGGTATNAANANGGCCATNNNTTNCANTNNC
CGNNNTGGGNTNCTTNTCATCNAGTNNCNATGGCGNGTATN
```

Figure 5-49

125C9-2 (7X)
fliP gene – Putative surface structure, flagella biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000287
Protein Accession # AAC75015

```
TACGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTITACCAAAATCATTAGGGGATTATCAG
GGCTGCGCCCTTTCCAGCGCCTCCTGCATTGATATTCTCTTCGCTGAATGGCTGGTACGCATCTACAT
AAATTGGTTCGATCACCGGTGACATAATAAAAAAGGTCAAAACAGTGCCAGCCCCAGCAATACCTGGTTA
GGTGGCGCGGAGGGTGTCCCAGCGCGTACGCAATAACCAAAACAATGATGATGCGGGTAAACTGG
TCATCATCAGTAAATTGCCGAATAAACGTCAACGAGGTGATGAACACCAGCGTCTGCACCGGGAGCGA
CCAGCTTGTCCACCGCCAGGCAGCGGCTGGCTGGTGTACCCGGCAGTTGCGCGAAGGCAGGGGGCTAA
TCAGCCAGAGAAGGACAGGTGCGACAGACAATAACGACGCAT
```

Figure 5-50

125F2-4(3.5X)
rfaQ gene (complement) – enzyme; macromolecule metabolism: LPS core biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_002695
Protein Accession # NP_312534

```
GNGNAAAAACGTNCCGG
ATCCGGATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTITACCAAAATCATTAGGGGATTATCAG
GATGGTGTCTGATAAACGAGCATATCGATTITGCATCANGATAATTCTGCTTGAGCGTACTGAT
GACAGGAGTAGTTAATAACATATCCCCATGATATCNCNNNCNNGTACTAGTCGACCGCTGGCC
A
```

Figure 5-51

126G2-2 (7X)
fliA (complement) - flagella biosynthesis; possible export of flagella proteins

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000281
Protein Accession # AAC74949

```
CGNCCGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTITACCAAAATCATTAGGGGATTATCAG
CCTGGTGCCTGGAATGCCAACCTGGTATTTGCTGTTCACTGCCGGATTGCTCGGGCTGGCTG
GTGGATACCGGGACCGAACAAAAAGCGCCTGCCAACCCAAACCGTAAAAATGGCAGAGAAT
AATACCGTTGTCGAAGCGACGTGGAACGTACAACCTGGAAGATTCTCTGGGAATGGAAGTGGG
TTAT
GGACTGATCCCGATGGTCGATTCCAGCAGGATGGTGAGTTGTTGGGCCGTACGCAGTATCCGC
AAG
```

Figure 5-52

126A3-2 (7X)
flhA gene (complement) - flagella biosynthesis, possible export of flagella proteins

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000281
Protein Accession # AAC74949

```
ACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGGATTCATCAG
CCTGGTGCCTGGAATGCCCGAACCTGGTATTTGCTGTTCACTGCCGGATTGCTCGGGCTGGCCTG
GTGGATACGCCGGACCGAACAAAAGCGCCTGCCAACCCAAACCGGTAAAAATGGCAGAGAAT
AATACCGTTGTCGAAGCGACGTGGAACGATGTACAACCTGGAAAGATTCTCTGGGAATGGAAGTG
TTATCGACTGATCCCGATGGTCGATTCCAGCAGGATGGTGAGTTGGGGCGTATACGCAGTAT
CCGCAAGAAATTGCCAGGAGATGGGATATCN
```

Figure 5-53

132B8-2 (7X)
fliM gene - surface structures/flagellar biosynthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75012

```
NTNNNAAACACGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGGATTCATCAG
CGTTTGCCTGCCATTTCGTATGGGGCTGTTCAACCTGCTGCCTGTAGCCCGATATCCNCCN
GGNGCGTACTAGTCGACCGTGGCCAANNNNNNNNNNCTAGCNNTAAAANNGNCATNANC
CNCNCNCAANCACNNANGNANNNCNTNCNAAACNANCNGTANNATANCCCN
```

Figure 5-54

136E3-1 (7.5X)
arcB gene (complement) - enzyme, Global regulatory functions, aerobic respiration sensor- response protein; protein kinase/phosphatase, sensor for arcA

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000400
Protein Accession # AAC76242

```
NNAAAGCCCGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGGATTCATCAG
CGCAAAGCCTGCTTGANATCCGTAAAGNGCGGACTAANCNACNCNGGGNCNAA
```

Figure 5-55

139G5-3 (5X)

rfaP gene – enzyme; macromolecule metabolism: LPS; phosphorylation of core heptose, attaches phosphate containing substrate to LPS core

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000440

Protein Accession # AAC76654

```
GNGAAAAAAACGNACCGGATCCGG
GATCATATGACAAGATGTATCCACCTTAACCTTAATGATTTCACCAAAATCATTAGGGGATTATCAG
GGTAAATCCATTAACTCGCGCATCATTATTACCGAAGATCTCACTCCCACAATTAGCCTTGAAGATT
ATTGTGCCGATTGGCAGTCAACCCGCTGATATCCNGNNCNNNGTACTAGTCGACCGTGGCCATANAN
TNAGCTCNTNCTACNNCCNNANTCCTATCCACCCGTGGCTNCAGNNANCATTNGNNNACACCANTTACNN
NCCAGNCCNCNTCCCCNGNNCTNNCTACTCANNACTTCANNANANNATNCNTTNNNNNGNNNTCGNT
CNCCCACNACNNCTTNTNCNNCTCTNNCNANCTCNCCNTNNCTNTNATTCCNCTTACCCCTNAN
```

Figure 5-56

152B4-6 (9X)

flgl - flagella biosynthesis, putative surface structure; product is homologue to P-ring of flagella basal body in *Salmonella*

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74164

```
GNNGAACGNCGGATCCGG
GATATATGACAAGATGTATCCACCTTAACCTTAATGATTTCACCAAAATCATTAGGGGATTATCAG
CACTTGCATTGATTGCACTATGGACATCAGATCCATCGCGTAGCGCCCAGCGCATTGAGCGCCG
GCACCACTGTTATTGAGGCTGGCGCTGGAACGTACGCTTGCAGCGAACCGCCGCTCTGGCGTAAAT
CGATCTGCGTTGTGGAGTAACCACAGTCTGTCCACCACCAAAACGGTGTATCTGGCTGGCTGACAT
TGGCTGACGATTAACGTAACTGAGAGATTCCCTGCCTACCGCGAGCTGTCGAGGGTCACCTT
CGCGATTCACTACCAACCGAACCGGTGCGAGTTAACACTACTTTAGC
```

Figure 5-57

163E7-5 (4X)

fliD gene – flagella surface structure; capping protein (same clone as 1B10)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

```
TNGAAAAACGTNCCGGATCCGG
GATCATATGACAAGATGTATCCACCTTAACCTTAATGATTTCACCAAAATCATTAGGGGATTATCAG
GGTCAGGTCTGGATTTAACGTTCCATCCTTGATAGCCTCACCGCCGCGCAAAAGCGACGCTNACCC
CCATTCAAATCAGCAATCGTCGTTACCGCTAAACTTAGCGCTACGGTACGCTAAAAGCGCGC
TGACGACTTCCAGACCGCCAATACTGCATTGTCTAACGCCATCTTTTCCGCCACCAAGCACCA
CCAGCAGCACCAACCGCGTTCAAGTGCACCACTGCAGGGTAACGCCATGCCGGAAATACACCATC
AGCGTCACCCATCTGGCGAGGCGAAACCCCTGACCACGCGACCACCAAGAGACGATACGAAAAC
GGCGATCGCCACCAGCGACAGTAAACTCA
```

Figure 5-58

163F3-5 (8X)
fliD gene – flagella surface structure; Capping protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # [AE000285](#)

Protein Accession # AAC74991

```
NNANNAACAATAACGTCC
CAAGNANANNTGACNAGANGTGATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTACATCNG
GGNCCGGTCTGGATTAAAGTTCCATCCTTGATAGCCTCACCGCCCGCAAAAAGCGACGCTAACCC
NCCATTTCANATCAGCAATCGTCGTTACCGCTAAACTTAGGCCTACGGTACGCTGAAAAGCGCG
CTGACGACTITCCAGACCNCNAATCTGCATTGTCTAAAGCCGATCTTTTCCGCCACCANCACC
ACCTGCAGCACCGACCACNGCGTTCANTGCCNCCNTGCGGGNNACNCATGCCNGGAAATACCCCAT
TACCGNTCANCCATCTGGCANATGCNGCNAACCCTGAACACCGC
```

Figure 5-59

167C2-3 (8.5X)
flgB gene – Structural component, flagella biosynthesis ; cell – proximal portion of basal body rod

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74157

```
AAAACGTCCGGATCCGG
GATCATATGACAAGATGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTACATCAG
CGCTCAATCTGCGCGCCCGCGTCAGGAAGTGCTGGCAGCAAACATGCCAATGCCGATAACCCCT
GGTTATCAGGCGCGCGATATCGATTTGCCAGTGAACCTAAAAAAAGTCATGCAACGTGGACGGGA
TGCAACCAGTGTGGTTGCAGTGACGATGACCTCAACGCAACACATTCCGGCGCAGGGCGCTGACGC
CTCCTACCGCAGAACTGCAATACCGTATTCCGGACCAGCCTTCGCTTGA
```

Figure 5-60

1G3-6 (16X)
ycdQ gene (complement) - putative enzyme homologous to IcaA in Staphylococcus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # [NC_000913](#)

Protein Accession # NP_415541

```
ATAAAACGGNTACCGGATCCGG
GATCATATGACAGATGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTACATGAG
GGCGCTGTTCCACAGCCCCTTTAACGTTTCAGGCATTAATATCCAGCACAGTGNCCTNGNNNCNNNN
NNCNTCCACTGATTCAACTGCAGCTCCAGCTAATATCAATATCTCGGTGATCATATNAGTCCACNCGGNN
CTAGTCGACCGTGGCCANNANTNNNNCNTNTNTNNCTN
```

Figure 5-61

11E4-3 (12X)

Immediately Upstream of promoter (factor sigma 70, predicted 1+ start site 1986220) and gene b1904 (orf, function unknown)

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NA (Not Available)
Protein Accession # NA

```
TTTAAAAACCGGTACCGGATCCGG
GATCATGACAAGATGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGATTATCAG
TGCCAGGCGTCTTCCGGCATTGTCGACGTAAACGCGTAAATAGTGCCTCTCTACTCTCTGGC
TGGACCATGAGACTTCTGATTCTGACTCTTCATTAATATCCNNNCNNNGTACTAGTCGACGCGTGGCCA
NANNANTNNTATNTTNANNACNN
```

Figure 5-62

12F12-6 (23X)

ycdS gene (complement) – putative outer membrane protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74109

```
TTGAAAACCGCTCCGGATCCNG
GATCATGACAAGATGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGATTATCAG
CGTTAAATTGGCATCGTCATCGCGGAGCAAGTTGATTATTACGTAATGCCTGCACGTAATTCTGTGGATA
TCCNNCCNNNCGTACTAGTCGACGCGTGGCCATNTACNTNCNGCAATNCNTCTGACACTCENNNTNC
TNTNNAT
```

Figure 5-63

14B7-4 (4X)

leuO gene –putative regulator; probable transcriptional activator for leuABCD operon; amino acid biosynthesis: Leucine

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000118
Protein Accession # AAC73187

```
GCNNNGCGTAAACGNCCGGATCCGG
GATCATGACAAGATGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGGGATTATCAG
AGTTAAGTGTGACAGTGGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGA
GTTAACGAAACACANCTTNCGNATGGNCATTCAACTTATTACNCGTTGATGCCNTGNTGN
AGGAGCCNANCATTNTTCNCAGCCCGCTATGCCCTGGAACCTTCNCCCCCCTNCNTTCTNT
GCTNGCCTTGGGGCCCCNNACNCAACGNAGACNGGGCCNATCCC
```

Figure 5-64

16C8-2 (24X)

Promoter (factor sigma 70, predicted 1+ start site 1986220); upstream of b1904 (orf, unknown function)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

```
AACCGTACCGGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACITAATGATTITACCAAAATCATTAGGGGATTATCAG
TGCNACGNCTNTNANNNCATNGATNTNGCACTGTAACGCGCTAAATAACGCTTGTNTCTTACT
CTTCTGGCTGGACCATGAGACTTCTGATTCTGACTCTTCATTAATATCCCCCNCCCGTACTAGT
CGACGGTGNCNATATTATGNNNCCNNNNCTANTNNNC
```

Figure 5-65

24E12-4 (8.5X)

fucA gene (complement) - enzyme, degradation of molecules: carbon compounds: product is L-fuculose-1-phosphate aldolase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000363

Protein Accession # AAC75842

```
CNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACITAATGATTITACCAAAATCATTAGGGGATTATCAGAG
GCAAGTGTCAATAATCTGACGAGCAAGTTATTCGTTCCATTAGCTACCTCTCTGATTCAAAC
AGGGCAATAATGTTGTTCCCTTCACACTATTGAATTAGCCGTTAATTACCCACCATTTCTTCTG
ATTAACAAGAAAGAAATTACAAGCTTATAT
```

Figure 5-66

26G11-3 (8X)

ycdS gene - (complement), putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000363

Protein Accession # AAC74109

```
AACGNCCGATTCCG
GATCATATGACAAGATGTGTATCCACCTTAACITAATGATTITACCAAAATCATTAGGGGATTATCAG
CCAGATGCGTTCTGACCCCTAAGTGAAGACTTCATGACGCTGGTTACTGTCCGAAAAATCAGTGAA
AGCCCAGGAGACACCGTACTTACGCCGCTCATTTGATACCAGCGAACATAAGCCTGAGCACTGTT
GCCTGTAACACCATTTTCAATTGCCGTAATGGAACGCCGAGAGAGAGGCCGTTCCAGTTGCGAAC
AATACGCCAGTTATCATTAAATCATACCAGCCAGACAGGCCGCGCCGGTTATGCTCATGATT
GAAAACGCCGTTCAAGCGTACTCTGCCTCGAGCCAGATATTACG
```

Figure 5-67

27F9-2 (2X)

Between promoter (factor sigma 70 predicted 1+ start site 4272977) and yjcC gene (orf; unknown function)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

```
AACGNCCGGATCCGG  
GATCATATGACAAGATGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG  
TGCCCAGGGTTTCACCTTGCATGCCGGGTATAAACAGGCAGGAAATTGANANCANTGAGNCA  
TNNNCAGANACCAATTNCTGGCNTNGCCGGCATTATCTTTTAATTCTCTTCCATCATTCTT  
TCGCTATGGATTGCCTTCCTTGGGAAAATCAGAAGTGAATAATCAGCTCCGAACCTTGCTCAA  
CTGGCACTGGATAATCCGAGCTGGTCATT
```

Figure 5-68

31A4-4 (7X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

```
CNCGCCGGACATCCGGATCCGG  
GATCATATGACAAGATGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG  
GTGACAGTTAGCCGCCGGATAATTTCACCTCCAGGTGGCTGTAAAAGAGATCCGCAAGTTCT  
TCATCGGATAAAATCCGGGCAATGGTCTCCTTGTGATAAAAGAGCTGGTCATTATTGACTGTGCT  
TTTTCCGGCTGATGATCTTGAGATAAGCCGATGCAACCCAATATTGCCCCAGGGCGGAATAATT  
TGCCCCGTCTTTTAATCGCTGATAGTGAGAAAATAACGTCTTATAACGATCGCGAGTTAAC  
GCGCCAAGATGATCAACCTGAATACGCTGGTACTGGCAGTGCAGCTGGTTATCGTGCCACAG  
AATTCTAATG
```

Figure 5-69

31G6-3 (2.5X)

Immediately Upstream of promoter (factor sigma 70, predicted 1+ start site 1986220) and gene b1904 (orf, function unknown)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

```
AAACGACCGGACCG  
GATCATATGACAAGATGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG  
TGCCNGGCGTNTTNCGGCCATTGNCNCAGCACTGNNACGGTAAAATAGNGCTTCTCTTACTC  
TTCTGGCTGGACCATGAGACTTCTGACTCTTCAATTATCCCCCCCCCG
```

Figure 5-70

32A4-2 (14X)

Between ptrB & yebE (complement) - ptrB gene - protease II; yebE gene -unknown function

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

```
NGANNATACGNCCGATCCGG
GATCATATGACAAGATGTATCCCTTAACCTAATGATTTACCAAAATCATTAGGGGATTATCAG
GTTGAAACATCTTATAAGGGGTGGCAAAACTCACCGGGATGCAAGCGAAACAGGGGAGTCATTG
CTTAGATGATGACAGGTAATGGCGCGGATATCGAATGTTATGCAANCAGANAANANCAGNCTGTT
CAAATGGCTGTGCGATTCTGGATAGCCGAAATAGTCAACTTCAGGCTATCCAGAGAGCGGAATT
ATTCCGCCAAAGTGCCTTGTGCTGAGATCGCGTTCAATGCCGTACCGAACATCTGGGGGA
TTTCAGCGCGTACCCAGTCATTCAAGTAACTCAGGTTCCATAAAATGGTCAATATCAATAGCCG
CGNNACTAATNNACNCNGGCCNAGCGCCTTTC
```

Figure 5-71

35C6-2 (6.5X)

hscA gene (complement)- factor, chaperone; product is heat shock protein chaperone, member Hsp70 protein family

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000339

Protein Accession # AAC75579

```
CGNCCGGATCCGG
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGGATTATCAG
TGCCGACGGTCTTTGAGCGTGACGGCGATGGAGAAATCCACCGCGTTGAGGCCTATTCAAGGT
CAAACCGTCTACGGTCTGACCGATAGCGAAATCGCTTCGATGATCAAAGACTCAATGAGCTATGC
CGAGCAGGACGTAAGGCCGATGCTGGCAGAACAAAAAGTAGAAGCGCGCGTGTGCTGGAA
AGTCTGCACGGCGCGCTGGCTGCTGATGCCCGCTGTTAAGCGCCCGAGAACGTCAGGTCATTGAC
GATGCTGCCGCTCACCTGAGTGAAGTGGCGCANGCGATGATGTTGACGCCATGAACAAGCGAT
TAAAAACGTAGACAAACAAACCCAGGATATCNCNNNNNCNGTACTAGTCGACCGTG
```

Figure 5-72

37B5-2 (11X)

yedK gene - hypothetical protein, function unknown

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74998

```
NGAAAACGTCCGGATCCGG
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGGATTATCAG
CTCCCGGCCCTGGTTTAACATTACCCACCGCGCGCGATATCNCNNNNNNNNGTACTAGTCGACG
CGTGGGCCAANTANNNNNCNNNNNTNNNNNNNCNNNTNNNNNGNNNNNCNC
```

Figure 5-73

41G10-2 (10X)

leuO gene - putative reg of AA biosynthesis (leucine) - Same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

```
AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCTCATCAG
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAG
TTAACGAAACACCACAGCTACGCATGGTCGATCTCAACTTATTAAACCGTTTCGATGCCGTGATGCAG
GAGCAAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCCCCCCCNNCNGTACTAGTCGACGCN
GN
```

Figure 5-74

41B10-5 (9X)

leuO gene - same as as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession #AE000118

Protein Accession # AAC73187

```
AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCTCATCAG
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAG
TTAACGAAACACCACAGCTACGCATGGTCGATCTCAACTTATTAAACCGTTTCGATGCCGTGATGCAG
GAGCAAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCCCCCCC
```

Figure 5-75

44C2-1 (10X)

ycdS gene (complement) - same clone as 31A4-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession #AE000204

Protein Accession # AAC74109

```
CNCGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCTCATCAG
GTGACAGTTAGCGCGCCCGATAATTTCACTCTCCAGGTGGCTGAAAAGAGATCCGCAAGTTCT
TCATCGGATAAAATCCGGGGCAATGGTCTCCTTGTGATAAAAGAGCTCGGTCAATTATTGACTGTGCT
TTTTCCGGCTGATGATCTTGAGATAAGCCGATGCAACCCAATTGCCCCCAGGGCGGAATAATT
TGCCCCGTCTTTTAATCGCTGATAGTGAGAAATAACGTCTTATAACGATCGCGAGTTAATAAC
GCGCCAAGATGATCAACCTGAATACGCTGGTACTGGGCAGTGCGGTCT
```

Figure 5-76

46E5-5 (10X)
ycdQ gene (complement) - putative enzyme homologous to IcaA in Staphylococcus

Transposon Tn10 Accession # AY528506
Nucleotide Accession # [AE000204](#)
Protein Accession # AAC74109

```
AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG
GAGCTGGNGCGTTTCTCCCCACGGCCAGTGGCGTTCACNATAGACCCAGAAATAGACGCCNCACAATN
CACATAATGGACATAAAAAACGGCCAGAAGAAAACGAACCTNATCATCAGTTCACCGAGTGAAAGTACGC
TACGCATAGGGTATGCATAACACCAGACATAATATAAAAACGATAACGATGCGATTAA
```

Figure 5-77

48A4-5 (20X)
trs5_11 (complement) - IS,phage, Tn; transposon related functions, IS5 transposase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # [AE000427](#)
Protein Accession # AAC76530

```
GAGATACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG
TGCTCCACCTGGCCCGGATGCTGGCTTCATGATTCGATGTTGATGCCGTTTGTCTCGTG
GATGCTGTTCAAGGTTCTTACCTTGCCTGGCGCTCGCGATCAGCCAGTCCACATCCACCTCGG
CCAGCTCCTCGCGCTGTGGCGCCCTGGTAGCCGGATCGGCTGAGACAAATTGCTCCTCTCCAT
GCAGCAGATTACCCAGCTGATTGAGGTATGCTCGTTGCCGCGTGGTAGCCAGGCTGTGGGTCA
GGCCACTTTGGCATCGACACCAATGTGGGCCATGCCAAAGTG
```

Figure 5-78

49C2-1 (9X)
ycdS gene - (complement), putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # [AE000204](#)
Protein Accession # AAC74109

```
CGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG
GATGAATTACGGCGATGACAGAGTCATTACCTGAAATGCATCTACGCAACAATATCCACNNA
NTNGTACTAGNCAGCGTGGCCATCAACTTGTGCCGCGATTGACGATGCCAATTAAAGGCCAGA
TATTGCGCTGATATTNCTANNCGACGNGCNGGNGACGCGTGGCCAANGCNNNCNTNNCTNN
NAANNNTGNNCNGNNCCTGGCTGNTGTCCNNNCTGNNNANCGCCNACANAACNTCNTGNCNTNN
NNANGCTGNGTCCCTTANNGAAGNGGCCNNGGNAATNATGTNNACNCNTNNCCAANCNTTN
NNNACTNNACNANCNACCCNNGATNTC
```

Figure 5-79

49G12-3 (20X)
ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74109

```
CACGGATCCGG
GATATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
CGTTAAATTGGCATCGTCAATCGCGCAGCAAGTTGATTATTACGTAATGCCTGCACGTATTCTGT
GGGATATCCNNCCNCCCGTACTAGTCGACCGTGGCCATGNATNNNCCGNATTATNCTGAT
GACNCCCCGNCAGTTATANATATNNNNNNNNGTNCT
```

Figure 5-80

51A10-4 (2X)
modC gene – ATP-binding component of molybdate transport; Transport of small molecules: Anions

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000179
Protein Accession # AAC73852

```
AACGCACCGGATCCGG
GATCATTGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
ACTGACCGCGCCCGCAAAAGGGCGGATTGTCTCAATGGGCGGGTACTAAATGATGCCGAAAAGGTATC
TGCCTTNCCTGACTAGTCGACCGTGGCCACNNNTTCATTNCNCCTANCTCNAAGTNNNCCNACTCCGN
GNNCNACCNCCNNCCNCCNTNGCAGNCNTGNCNNACNNCCGNACCCNNNGANNNCNCTCCNCC
GCCCTNTCNCACCTNNNANGCNTACCNGCCCCTCNGCTCNGTTACCTTNTNNNTNNCCGNCCCN
CTCANANNCCNTNACNGNCNNCATTNCNTCGCNNNNAGTANNCCNCNTCCCCCACNCNCNNN
CCGTNTTNCNCTTGANCT
```

Figure 5-81

56C11-1 (5.5X)
modC gene – Same clone as 51A1-4

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000179
Protein Accession # AAC73852

```
AACGNACCGGATCCGG
GATCATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
ACTGACCGCGCCCGCAAAAGGGCGGATTGTCTCAATGGGCGGGTACTAAATGATGCCGAAAAGGTNTC
TTGCCTGNCCCGTACTANTCGACCGTGGCCAACNAACCTNCTTNTCGNNTCCCTCNGCNC
NTCNCNCCACTCCNGCTGCTCCTNCNNCTTCNCNCNTACNTCGTNNCCTTANTCCACCTGCNNCTA
TCCCNCGGCCCGNCCTCCGNCCCCCNCTNAANTGTTCANGNACNGNCNCCTCGCCNAGCGCTNC
CNGNGCCAGNNCTNTTCATNTCCCTCCNGATCCANTCNCNNCCNTNCNTCTNACNNCCNGTCNCTN
NCCCCCTNNTTAN
```

Figure 5-82

62C9-2 (20X)

yeCK gene (complement) - putative enzyme (cytochrome C type); not classified ,product homologous to TorC cytochrome of TorCAD resp. system

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000281

Protein Accession # AAC74943

CNCGACGG
GATATATGACAAGATGTATCCACCTTAACCTTAATGATTTCACAAAATCATTAGGGGATTCA
GGTTTCGCTGTCCTTTGTGCTTGTATGCATTCTGCGCAGATTCACTTGCAGGGCAATATCC
ATGGCATAAAANAATGGCAACTACGGCACGTTGCAGAGTCAGTGGCTTTAATTCTTCCATACT
GTTTCGGCATTCTGGCAGGCTCGAACCTATCGCACTGTCTATTGCGCTAACAAATT
CATGATAAAATATCTTAGATGC

Figure 5-83

63E2-3 (2X)

between genes *clpP* and *clpX* – *clpP*: enzyme; degradation of proteins; ATP-dependent proteolytic subunit of *clpA*-*clpP* serine protease, heat shock protein F21.5. *clpX*: enzyme; degradation of proteins, ATP-dependent component of serine protease, chaperone.

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AAACNNCCGGATCCGG
GATCATATGACAAGATGTATCCACCTAACCTAATGATTTTACCAAAATCATTAGGGGATTATC
GGTTTGACCCATGACAGATAAACGAAAGATGGCTCATGCANATTGCTTATTGCTCTTTGCGGCAAAA
GCCNNCATGAAGTGCGCCAGCTGANNAGCCGNCCATCCCTNTATATCNCCNNCCCTGTACCTNGNCGG
CNCGTGGNCNNNCTCTNTCTNNCNTCTCCCNNTCTNNNNCCCTCTNCGCGNCCNCTGANNCGC
CTCNCTCTNTACCTCCNCNGCCTTACCNCTCGNNCTCNCACCTCCCTATTCCNCCTCCNTCNT
NTCCNTCTCCACCTNTCTTCCNACCGCNCATNNNACGTCTCNTTCCCTNNNCCACNNNTNATCCTCN
GCNCCCTCNGNGCAANCNTCNCNNCTANCGGCNCNGTGNNCNTGCNNCNCANTNANCNCNCNTNA
TTGAGTGCNGT

Figure 5-84

66E10-1 (12X)

ycdS gene (complement) - putative outer membrane protein, same as above

Transposon Tn10 Accession # AY528506

Nucleotide Accession #AE000204

Protein Accession # AAC74109

CNCGATCCGG
GATATTGACAAGATGTGTATCCACCTAACCTAATGATTITACCAAAATCATTAGGGGATTCATCAG
GTGACGACATCCGTGCCATAATGTTTGCAGGAGGCACCAACACCTGCGCTGAATATTGCTCCAGCTA
TTTCACTAGCTTCGCCATAACAAATGGCTTGCTCAAATGCCGAAACAATATCNNNCNNNNNGTACTAGT
CGACGGCGTGCCA

Figure 5-85

68E11-2 (2.5X)

glnE gene (complement) – enzymes, translation and modification; Adenylylating enzyme for glutamine synthetase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000387

Protein Accession # AAC76089

```
AAACCCACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACAAAATCATTAGGGGATTATCAG
AGTTTATCTCGCTCTGGCGAACGCATTATGCATCTGTTAGTACCGTACCTCTTCCGGCATT
GTATGAAGTGGATGCTCGACTCGTCCGTCCGGCGGGAAATGCTGGTGACATCCGCAGAAG
CATTGCCGATTATCAGAAAAACGAGGCCTGGACGTGGAAACATCAGGCCTGGTGCGTGCCTG
GTAGTGTACGGCGATCCGAGCTCACCGCGCACTTGACGCAGTGCCTCGCAGATTATGACGCTG
CCCGTGAAGGTAACACTGAAACCGGAAGTGCAGGAAATGCCGAGAAAATGCCGCTCATCT
CGGCAATAAACATCGCAGTCGTTGATATCAAAGCTGATGAAGGGGAATTACCGATATCGAAT
TTATTACCAAT
```

Figure 5-86

68A3-1 (>24X)

wcal gene (complement) - putative enzyme, colanic acid biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_000913

Protein Accession # NP_416554

```
GNCNNCTAAAACNTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACAAAATCATTAGGGGATTATCAG
GGCCGNANGGTGTGGCGCTGCCGCTGTATGTGCCAAACAGCCGAGCACCCTGAAACGCCTGT
TGCATCTGGCGAGTTTGCCTCAGCAGTTCTTCCGCTATGGCGCAACGTCGCTGGAAAGCCGG
ATCGCATTATTGGCGTGGTGCACCGCTGTTGCCTGCGCCGGAAATGCCGCTGCTGGCGAAACTCT
CTGGTGCCTGCTGCTGCATATTAGGATTACGAAGTGGACGCCATGCTGGGGCTGGCCTTG
CCGGAAAAGGCAAAGGCCAAAGTGGCACAGCTGGCAACCGG
```

Figure 5-87

73E6-6 (16X)

ycdS gene (complement) – putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

```
CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACAAAATCATTAGGGGATTATCAG
CGCATCTGGTCTTCACCATATTGATTGTCGATTCCTACCCAGTCTGTATTACGAACAAAATACAG
AACACGATACCCCATACTACAAACCTATAAAACGTTCGATATNGTCCGGCNTGTGCTGCNCNC
NNGTGGNCTGGCGAACGCTATGAAAATAGCTGGGAGCAAATATTAGCAGCGCAGGTGTTGGCTCC
TGGCAAAACATTATGGCACGGATGTCGTACCCAACTCGGCTACGGGCAACGCATTAGTTGGAA
TGACGTGATTGATGCTGGCGAACGCTACGCTGGAAAAACGACCTTATGACGGTGACAGAGAAC
ACAACTTATACGTTGAATTGATATGACATTAGCATTAAAGGATAAAATATGTTACGTAATGGAAA
TAAATA
```

Figure 5-88

73E9-1 (12X)
ycdS gene (complement) - putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession #AE000204
Protein Accession # AAC74109

```
ACGNCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGATTATCAG
CACCGTACTTACGCCGCTCATTGATACCANCGAACATAAGCCTGAGCACTGTTGCCGTAAACACCATT
TCATTGCCCGTAATGGAACGCCGTGAGAGAGGCCAGTTGCGAACAAATGCCAGTTATCATTAAAA
TCATATCNGCCNGNCCNGTACTAGTCGACGCCGTGCCANAAATTGAAAAGTGGTTGCCANAATTNTCTNG
ATCNCTTAAAGCTATNACTGGACNCGNTATNATGGNTNTGNNTTATCTGGNANGGGNNNCANAAAAAA
TNCGNTGCCAATGGNTNATNCAATTGNCCATNAAATTAAAAACATCCCTTANGNTNAAAGACAAATNNATT
TTNTAATTCAAGGGCNA
```

Figure 5-89

73F2-1 (12X)
ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession #AE000204
Protein Accession # AAC74109

```
NNGNAAACCAGCCGACNTCCCGGATCCGG
GATCATATGACNAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGATTATCAG
NCAGATGCGTCTCTGACCCCTCAAGNGAGACTTCATGACGCTGGTTACTGTGGAAAAATCAGTGA
AAGCCCAGGANACACCGTACTTACGCCGCTCATTGATACCAGCGAACATAAGCCTGAGCACTGT
TGCCTGTAACACCATTTCATTGCCGTAAATGGAACGCCGTGAGAGAGGCCAGTTGCGAAC
CAATACGCCAGNTATCATTTAAATCATATCNCNGAAGAGGACTAGTCNACCGTGGCANNAC
ANCCNCACTNNTNAACNTGNGGCTACNANTNTACCNGCCANNAGNNTACNTNANTNCGCNC
CCTNCCANTCNCNNNNANGTNNNCNAANCTNNANNCTN
```

Figure 5-90

75E11-5 (1.5X)
moaC gene - enzyme, biosynthesis of cofactors, carriers: molybdopterin; molybdoprotein biosynthesis, protein C

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000181
Protein Accession # AAC73870

```
NNAANATACGGTTCCGGNTCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGATTATCAG
ATGGAAGCATTAAACCGCGGCCCTCCGTGGCGCGCTGACCATTTATGACATGTGCAAAGCGGTGCA
AAAAGATATCNCNNNNCCNNNGTACTAGTCGACGCCGTGCCAAANATCNGGNTCTCNNNTGCTN
GCTNCNAATCNANTGNACCCNCTNAACCCTTCAGCTAAACATNTNNATNTGNAACNNATAAAC
NCAGGACGNCACTATNGNGTNNACNT
```

Figure 5-91

84A10-6 (11X)

ycdR gene - orf, unknown function, product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # [AE000204](#)

Protein Accession # AAC74108

```
CGNNNGANACGNCCGAATCCG  
GATANTANACAAGATGTATCCCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG  
GGCTTAGCGGGAGTCTGAGCGAAATTGACAAAACCCGGAGCAATTAAACAGTGGGCCCGCTT  
TAAAAGTCGTGCGTTAACTGACTTCACTTAGAACTTAGTGCACGCGTAAAGCCATTGCGGGTCC  
ACATATTAAAATGCACGAAATATTTCGACTCCGTAATACAACCTGAAAGTGAAGCCTGGTT  
TGCACAGAATTATGCTGATTCCTAAAAGCTATGACTGGACCGCTATTATGGCTATGCCTTATCT  
GGAAGGTGTCGACGGCTGACCAATGGTTAACATTAATTGA
```

Figure 5-92

86E7-6 (10X)

ycdQ gene (complement) - orf, unknown, putative enzyme homologous to IcaA in Staph

Transposon Tn10 Accession # AY528506

Nucleotide Accession # [AE000204](#)

Protein Accession # AAC74109

```
NACGGATCCGG  
GATATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG  
TATCTGGTGTGCATTGATGGCGATGCGTTATTAGACCGCGATGCACGGCATATATTGTGGAACCG  
ATGTTGTACAACCCCGCGTGGGTGCCGTAAACCGGTAACTCGTATTGAAACACGTTTACCCCTG  
GTGGGTAAAATTCAAGGTTGGCGAGTATTCTCAATTATTGGTTGATCAAGCGAACCCAGCGTATC  
TATGGAAACGTATTACCGTT
```

Figure 5-93

86F11-6 (11X)

ycdQ gene (complement) - same clone as 86E7-6

Transposon Tn10 Accession # AY528506

Nucleotide Accession # [AE000204](#)

Protein Accession # AAC74109

```
NCGATCCGG  
GATCATGGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG  
TATCTGGTGTGCATTGATGGCGATGCGTTATTAGACCGCGATGCACGGCATATATTGTGGAACCG  
ATGTTGTACAACCCCGCGTGGGTGCCGTAAACCGGTAACTCGTATTGAAACACGTTTACCCCTG  
GTGGGTAAAATTCAAGGTTGGCGAGTATTCTCAATTATTGGTTGATCAAGCGAACCCAGCGTATC  
TATGGAAACGTATTACCGTT
```

Figure 5-94

87C5-1 (1.5X)

aroD gene – amino acid biosynthesis: Chorismate, enzyme; product is 3-dehydroquinate dehydratase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000264

Protein Accession # AAC74763

```
AAACNTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
CGGCAGCGAGGGCATTCCACCGAGGCTTATATCCCCCCNNCCGTACTAGTCGACGCCTGGCCAANTATC
NNGATNNCCCCGCCTGTCAANNANCCCCCTGCNCCCTCCTCCNACTCNANCNTAGACCNGCCNCTN
NTNNNNCANCTCNGGCNTGTNCCAACCTGCNCCNCCCTGCCTGCCACNCTCTCCACGNCCNCCNCCN
NTTNCCNGCCCTGCCNNCTCTCCCCCCCNCNCCACNCTCNGCCCTCAGNCNCNGTCCGCTCGTNCCN
CNACNCNNCNCNNNAGCTCTCCNGTTACCTCACCGATGNTCNCCTCGNGNGCNCACCCNNAGCAG
CCNCNTNNNC
```

Figure 5-95

89E11-5 (8X)

leuO gene – same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

```
AACGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
AGNTAAGCGTGTACAGTGTANTNNNCTACNGCCANAGGTACAAACAANTTCATNCATNNGCCGNGAAGA
TTTCCTTNTNNNAGCNCAGCCNNNTNTNNNCANTNTCTAACCCNTNNCCTGGTNGTNANNCA
NGTCATNNNCATTNANTGNNTNTCGANTNCGCNTCNC
```

Figure 5-96

90A11-6 (3X)

rnpB gene (complement) - Enzyme; Degradation of RNA/RNase P, RNA component; M1 RNA; processes tRNA, 4.5S RNA

Transposon Tn10 Accession # AY528506

Nucleotide Accession # P06277

Protein Accession # P06277

```
GNAAAGCCGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
AGCCGGAAGTNAACGCGGGCTGGAGAAGATGAAAACCTCTCANAAGCGATTATTCGGTGAG
TGGAAAGGNATACCGGCGAAGCAATCACTGACGTAGTGAATATCNCNCNCCNGTACTAGTCG
ACCGTGGCCACANNNNNNNNNNNNNNNNN
```

Figure 5-97

90E7-1 (2X)

aroD gene – amino acid biosynthesis, Chorismate; 3-dehydroquinate dehydratase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000264

Protein Accession # AAC74763

```
ACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGGATTATCAG
TGCTCGCCGCCTTCTTGGCACTGCGGAAGGTAACAGCAGCAGCAGCTTTCTGGCATGGACTCACGGAGAATT
TTTGCTGCCCATGACAGACTCCACATTGGAGNGGTANGCATNCTGGNCCACACNCCATTCCANANTATC
NNCTTNNCTGNACTANTNANNCTGNANTNTNCNTCNCNNNCNCNANTCCTCNCNNCTNNACNN
NCNGNNNNNTGTTGAANNNTNNNACANCNCANNTCCNCNTCTNNATANATNGNCCNNGCCTN
NNAGTNNTANTNCNNTTNNTC
```

Figure 5-98

91F9-6 (2X)

b2531 gene – orf, function unknown; hypothetical protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_000913

Protein Accession # NP_417026

```
CGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGGATTATCANCAN
GGGCCCGGTACCGTTGGCTGATATTCCGAACGTCAGGGAATTCCCTTCTTATCTGGAACAACTGTTTTC
CCGTCTGCGTAAAAATGGTCTGGTTCCAGCTACGTGGACCAAGGGCGGTGGTTATCTGTTAGGCAAAGATG
CCAGCAGCATGCCCGTGGCGAAGTAATTAGCGCCGTTGACGAATCTGTAAGATGCCACCCGTTGTCAGGGT
AAAGGCGGCTGCCAGGGCGCGATAAAATGCCTGACCCACGCGCTGTGGCGTGTATTGAGCGACCGTCTCAC
CGTTTCTCAACACATTACTT
```

Figure 5-99

93E3-6 (12X)

ycdR gene (complement)– orf, function unknown; product homologous to IcaB in *S. aureus*

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

```
CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGGATTATCAG
GGCTTAGCGGGAGTCTGAGCGAAATTGACAAAACCCGGAGCAATTAAACAGTGGGCCCGCTT
TAAAAGTCGTGCGTTAACTGACTTCACTTAGAACTTAGTGCAGCGCGTAAAGCCATTGCGCGT
ACATATTAAACTGCACGAAATATTTCGACTTCCGGTAATACAAACCTGAAAGTGAAGCCTGGTT
TGCACAGAATTATGCTGATTTCCTAAAAGCTATGACTGGACCGCTATTATGGCTATGCCCTATCT
GGAAGGTGTCGAGAAAATCGGCTGACCAATGGTTAACATGACCAATCAAATTAAAAACA
TCCCTCAGGCTAAAGACAAATCTATTAGAATTACAGGC
```

Figure 5-100

96B10-1 (11X)

nhaR - regulator, transport of sm molecules - cations; encodes a positive regulator for nhaA(a Na/H antiporter)
stimulates transcription of osm-c

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000112

Protein Accession # AAC73131

```
NCAACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTTAATGATTITACCAAATCATTAGGGGATTATCAG
GTTTATGCTGACTTAATTGCTCCAGCAGCATTCTGTGGGTGGATTGAAGCAGCGAAGATGAATGG
GCTCGCCTTCTACCACTGCCGCGTTAACGTACGCTACTGACCAGCGTTGGAAAGTGCATCAGCCA
CGCCAACGTCAAACAATAATTGGATTCTTGCATAGTTACAATATCCNNCNNNCCGTACTAG
TCGACCGCGTGGCCAN
```

Figure 5-101

102G9-5 (5X)

leuO gene – Same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

```
AAACNCACCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTTAATGATTITACCAAATCATTAGGGGATTATCAG
AGTTAAGTGTGACAAGTGGAGTTAACGTATGCCANAGGTACAAACAGATCATNCAGAGACGGNGG
AGTTAAGCAAACACAGCTACAGCATGGTCATCTCAACTTATTAAACCGTTTCGATGCCGTGATG
CAGGANCAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCNCNNNNGNNGNACTAGTTCG
ACGCGTGGCCNCATANNATGNTCENNNTCTCENNNTCTCENNNTGCTTCCTNCCCTCTTCCNGC
CCCCCANNNGTCTNNNTNNATCNGNNCTNNNTACGACTN
```

Figure 5-102

106B2-6 (5X)

leuO gene – same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

```
AAACCCNTNGGATCCNG
CATCATATGACAAGANGITGTATCCACCTTAACCTTAATGATTNTACCAAANTCATTAGGGGATTATCAG
AGTTAAGTGTGACAGTGGAGTTAACGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGTGGAGTTAAC
CAAACACAGCTACNGCATGGTCATCTCAACTTNTAACCGTTNTCGATGCCGTGATGCCAGGAGCAAAAC
ATTACTNCGTGCCGNTCATGTTCTGGGAATATCCCNNGNNACGTNCTAGTCNANGCGTGGCCAANNGNTN
NGGNNNCTNANTCACAGNANCTTANNNGTN
```

Figure 5-103

109B4-4 (2X)

Between two protein binding sites (complement) - 1)central position to predicted promoter: -0.5/LexA predicted site and 2)documented IrP site/ central position to leuABCD promoter:- 156.5

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

```
AGCNCGCCGACNTCCGGATCGG  
GATCATATGACAAGATGTATCCACCTTAACCTTAATGATTTTACCAAATCATTAGGGATTATCAG  
TCGGTAGTTAACGAGAAATTAAATATCGCTTACTTTAACCCACCGCAGCACAATTAGCTAATTTACG  
GATGCAGAACTCACGCTGGCGGGACGTTTATTGCGTCAGGGTTGACATCCGTTTGTATCCAG  
TAACTCTAAAGCATATGCCCCCNCCNGTACTAGTCGACCGTGGCCANAACNCGNNNTCCAN  
TNTNNCC
```

Figure 5-104

110G8-2 (9X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

```
GNAANGAAAACNCGCCGACATCCGGATCCGG  
GATCATATGACAAGATGTATCCACCTTAACCTTAATGATTTTACCAAATCATTAGGGATTATCAG  
NACNGCNNATTGNNNCCACGGNGGANTAANTNGCCCNNGNTGNNTCTCGCTGNTAANGANAAA  
TAACGTCTTATAACGANCAGCTNAATAACCGCAGATGATCAACCTGAATACNCTGGTAC  
TGGGCAGTGCAGCTGGTTATCGTGCACAGAATTCTAATGCAGCGTATTGGCGAGGGCGCG  
ATCGGAATGGCATAACGNTCACTTCACTGCGTAGGCATAAACGACAGTCTGACCAGTTCGGC  
ATGAATATCAGNNNTGNTGNACTAGNCACCGTGGNCAAAACAT
```

Figure 5-105

115C12-5 (16X)

ycdR gene (complement) – orf unknown function; product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

```
CGNCCGGATCCGG  
GATCATATGACAAGATGTATCCACCTTAACCTTAATGATTTTACCAAATCATTAGGGATTATCAG  
AGCTTAATACCGGCATCCACGCATAATGTTTACACCTGAGCGGGTACGTAATTGCCAGGCAACCC  
GACTAAAAATATCTGCTTCATTGGNCTNACAAACNGGGANCCAGACCTTTGACCAGCCAT  
CACCATCGGGATCAGCAAATGCCTGCAAATACACGGTTGATATTGCATATCTTCCCCNCGTAC  
TAGTCGACCGTGGCCACATTACTNTANTNTANNANTGGATCCNANTNANNCGNTNTANCTNG  
CCTTGNANGGNGNNANNATTATCNNTGCCNNCGACNAANT
```

Figure 5-106

123F5-6 (4X)

modA gene - transport, small molecules: anions; molybdate-binding periplasmic protein; permease

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000179

Protein Accession # AAC73850

```
TITNNNGAACACGCCGNACATCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGGATTCA  
TGGATTATGCGGTTGATAAAAAAGCGATCGATACAGCTACGCGTCAGACACTGCTCGCAATAGC  
CTGGTCGTTGAGCACCGAAAGCCAGCGTGAGAAAGATTTCACCATCGACAGCAAAACCAACTG  
GACTTCACTGCTGAATGGCGGTCGCCTGGCGTTGGCGATCCGGAACATGTTCCCGCTGGCATT  
TGCAAAAGAAGACTGCNAAAATGGCGCATGGGATACNCTCCTCGAAAATGGNCCNCNTA  
AGNTGNTCTAGGGNNNCNNCGCNGGTACCCACNTAATCGAACCN
```

Figure 5-107

125A7-1 (2.5X)

rbsK gene - enzyme, degradation of small molecules: carbon compounds; ribokinase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000452

Protein Accession # AAC76775

```
GCAAAACGANNCGGCCAAG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTACCAAAATCATTAGGGGATTCA  
GAAAGGGCAGCNTTANCGCCGGCATGAATACCGATGACATTCTCACCTCGCCATTAACAAAAAT  
CANCGCCACACCTGTTGATTGCCTTGATCTCGCTGACCGGAGTAANATCCCNTNNNNACTA  
GTCNACGCGTGGCCATNAANTCENNCGACCNTANGACCCNANTCCTGNNNTTAANNNCNCNN  
CCNTANTTGCNCANNNN
```

Figure 5-108

125E4-1 (24X)

insB_4/insA_3/insA_2 genes (complement) - all three have the same probability score and identities, 89% -
IS, phage, Tn; transposon-related function

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

```
CACANCCGNACATNCGC  
ATNNCTACTNANAATGNCGTGAANTATTNCNACTGCNTNACACTTACACCGNNCTCATNCGGTANGC  
ACACACANAAANNTGAAATATGAGGCATGAATGGTNGTGGANGCCGGTAACAGCCNTCATTATG  
GGNGTTGGCCTCAACACGATTTCCCTCCNTTAAAAAAACTCACGCCNTACCCGTAAACCTCGCAC  
CATACTGGCAGGGCAGCNGACNGATTGCCTGCGCATGAAATGNANAAACNNTGGGATNCACCA  
GGGNGTAAATCTNGCCAGCGATNNCTGNNTNNCTTNTGANANGATNCNGAAAANGGGGNTGC  
NCNCGTNTNCCGGNAAACATCNNTAATAAAACTGGGGCAAAGTAAAACGTCNGGATATCCAATC  
CANNNGTACTANTCGACGCGTGGCCANNACTGNC
```

Figure 5-109

126C5-4 (7.5X)

leuO gene - same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

```
NNACGCTNCGGNNCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAN
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAG
TTAACGAAACCACAGTCTACGCATGGTCGATCTCAACTATTAAACCGTTTCGATGCCGTGATGCAG
GAGCAAAACATTACTCGTGCCGCTATGTTCTGGGAATATCNCNNCTNNNGTACTAGTCGACGCG
TGGCCANN
```

Figure 5-110

130E8-4 (24X)

Between yecK and cutC genes (complement) - in a protein binding area with no predicted promoter; TyrR predicted site

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

```
ATNCNCACCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAN
NGTCCAGTAATTCAATTANAGGAATCTATGCGNGGGANAAACGGNTGGCNGCTNCNCGCTAANGC
NAANAANTAANCCNCCTNNNCTANGTATNNNNNGNCNTNNNANNNCNGNTTCT
```

Figure 5-111

130G11(2.5X)

aroD gene – enzyme: amino acid biosynthesis: chorismate; 3-dehydroquinate dehydratase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000264

Protein Accession # AAC74763

```
ANNCNNCGACCGN
GNTCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGATTATCAG
TCNGGCCGANCNGCNATTCCACCGAGGCTTATNTCCNCNNNTNTCGNNCTAGNCNNNGCNTGG
CCANGTTNCGNCCNNCTNACNCNCTCCATNANTNTNNCCNTNCNNANTACNGTGCCGN
GNATNCCNTCCGTGGCCCCCNNGCTTAGCNGCNAANTGGCCNNNNCAANTTANGAC
GATCNGCNGCCNNTAACNGNGTTNGCCATNTNCNTNCNTTTATN
```

Figure 5-112

140B5-1 (9X)

miaA gene – enzyme, Aminoacyl tRNA synthetases, tRNA modification; delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000489

Protein Accession # AAC77128

```
CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACITAATGATTTTACCAAAATCATTAGGGGATTATCAG
AGGCAAGTCGTATGCAAATCTCCTCGGGCAAAAGCGCCCGGACTTCTGCTCAAAACCTGAAG
CCAACATCTGATGAAAACGCTGCTCAATGCGTTGATGGAGCAGITCAGGGCTCGCCGGGGCGATG
GCGAACTGATGCACCTGATACGGTAGAGCGTCTCCTGACGTTGCGTCAGTTCCGTTAAAGTTTA
CCCGAAATGAAAAAAACTCCAGTGCCCAGGAAAGCCTTGTGGATCATTTGGATGAATCCTTGCT
GCCGCAACCGGATCTACCTCCTGAAGTTGACGATGCAATGACTCCAACCTGCTCTGCCGCCTGT
TGCTCAATTCTGGCCCGTACTTCCGGTCTGCCGACGGTAGCGCGACAACCCTCCAGCAATGCC
TTGAAAT
```

Figure 5-113

141G2-2 (16X)

yjjQ gene - putative regulator, not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000507

Protein Accession # AAC77321

```
GNCGGATCCGG
TATATATGACAAGATGTGTATCCACCTTAACITAATGATTTTACCAAAATCATTAGGGGATTATCAG
GATGGGGCATCAACCAGATAGCTTCATTGCTTAAGAAAAGTAATAAAACTATCANCGCCAAAAAA
AACAGTGCATGCGTCGACTGGCAATTCACAGCAACGCTGAAATGTATGCATGGATAAATAGCGC
GCAGGGTGCAAGAGAACTTAACTTGCCTCTGTTATGGAGATGCCGAGAATGGAACACAGCCG
ATTAAGAAGAGAAATGTCGCACTC
```

Figure 5-114

141G4-6 (18X)

ycdS gene (complement) - putative outer membrane protein; not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

```
NNAAAGCAGCCGGACATCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACITAATGATTTTACCAAAATCATTAGGGGATTATCAG
ACCCAATATTGCCCGAGGGCGGAATAATTGCCCCGTCTTTTAATCGCTGATAGTGAGAAATA
ACGTCTTATAACGATCGCGAGTTATAACCGCCAAGATGATCAACCTGAATACGCTGGTACTGGG
CACTGCCTCTGGGTTATCGTGCCACAGAATTCTAATGCAGCGTATTGGCGAGGGCGCGATCGG
CAATGGCATAACGTTCACTTCACTGCGCGTAGGCATAAACGACAGTCTGACCAGTTCGGCATGAA
TATCANC CGAATAGTACTAGTCGAC
```

Figure 5-115

145F10 (3X)
ykgK gene (complement) - putative regulator; not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000136
Protein Accession # AAC73397

```
NNNNGAAGCNCGCCGACATCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTITACCAAAATCATTAGGGATTATCAG  
TACCAACGCCCTAAATATTGCTATTGTAATACCAATAATTGCTAAGGCCTCTGACTTCTGGCCGCA  
ATCAATACGACCTGTTCCCTTACCGCGATAACCATTATTACCGTTATAAAATTAGATA  
AAGAATCCGTACTGAGATTGATAAACACGAATCTTTCTAATTCTCAACGATAGATAAATT  
ATCTGTCGATATCCCCNNNGTACTAGTCACGCGTGGCCA
```

Figure 5-116

150E3-6 (20X)
ycdP gene (complement) – orf, hypothetical protein unknown function

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_000913
Protein Accession # NP_415540

```
NACGACCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTITACCAAAATCATTAGGGATTATCAG  
GGCCAGAAGCCGACTTCAGTTCTATTGCTGGCAGTGGCGAATGCCGTGTTAATTGCTGGCGCT  
GTACAATAAGCTCGTTTCAAAACAGCAGCATCATGCAGCCTACCAATATACGCCAAGAATATGCAG  
AGAGCTTAGCAATACCTGATGAGCTCTATCAGCAACTACAAAAAGCCACAGGATGAGCGTACACTCACC  
AGCCAGGGGCAAATAAAATGGTTGTTCAGAAAAAGCGCTAGTCCGGGCATAAACACCCAAAACAAAGC  
CCGGTTCGCCCCGGCTCTGCACCGATAACACACTTAACGTAGGCATGCAGCGTACGTTGGCAAAGTGGCG  
AACGTACGCANT
```

Figure 5-117

150G7-2 (4X)
prfC gene- Factor; protein translation and modification; peptide chain release factor RF-3.

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000508
Protein Accession # AAC77328

```
ANACNCGTCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTITACCAAAATCATTAGGGATTATCAG  
TGTGGTGTCCGGTAAATATGAAAAAGGCATNAAACTGCNCCACGAGCCCCTGCNAANGATGNGG  
NAATCTCCGCCCGCNGCCTCTGGCNGGTNNCCGTTCTCACCTNNACACCNCNNNGCTNC  
NTNCNCTCCNNACNNCNNTCTCTCNGCANCCACTTNATCTNCCNNCCCTCCNACGNNT  
CCNCCCNCGNNNCANTGNNTGGCTNNCGNCCNNNNNCNCNCTCNCNTCCCTGCCTCNCNT  
ACNCNN
```

Figure 5-118

155F4-4 (20X)

ycdR gene (complement) - orf, unknown, product homologous to IcaB in *S. aureus*

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

```
NNCGATCCGG
GATCATTGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
CACTTGTGCCACGTGGCAAAATATTCTCGATCGACCAACTCATGCCAAATTTACTGTATCC
GCTGGCATATCNCCCCNNNCGTACTAGTCGACGCGTGGCCANN
```

Figure 5-119

160A8-6 (20X)

yjjQ gene – putative regulator; not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000507

Protein Accession # AAC77321

```
CGNCCGGATCCGG
GATCATATGACAAGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
GGCATCAACCAGATAGCTTCATTGCTTAAGAAAAGTAATAAAACTATCAGCGCCCAAAAAACAG
TGCATGCGTCGACTGGCAATTACAGCAACGCTGAAATGTATGCATGGATAATAGCGCGCAGG
GTGCAAGAGAACTTAACCTGCCCTCTGTTATGGAGATGCCGAGAATGGAACACAGCGAATTA
AGAAGAGAAATGTCGCACTCATAGAAAATGCGTCATGAGTAGTATCGGTATTGAGAGTTATT
AGAAAGTTGCGGGTAACCTTATAAGCTCCATACCTATACCGTCAGGAGTCATTTCAGGATGCC
ATGTCGCGGATATCCNNCCNCGTACTAGTCGACGCGTGGCCAA
```

Figure 5-120

169G4-6 (18X)

ycdR gene (complement) - orf, unknown, product homologous to IcaB in *S. aureus*

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

```
AAAANCGCCGGACATCCCGGATCCGGATCAT
ATGACAAGGATGTATCCACCTTAACCTAATGATTTACCAAAATCATTAGGGATTATCAG
TATTAATGCCAATAATCCCTCATTAAGAGTTGCCAGCAAATTATTACCGTACAGGAAAAAT
CACCACAAACGGATAATGCATATCNCNCNNNNNGTACTAGTCGACGCGTGGCCACANAN
```